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Listing first 45 summaries
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Matches 33; Conservative 551; Mismatches 267;
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17-MAR-2000; 2000US-0190259
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electron-transfer group,
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                                                                Example 6; Page 127; 159pp; English.
                                                                                        for genotyping, allowing repeat analyses
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The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression. two nucleic

Sequence 936 BP; 5 A; 142 C; 7 G; σ Ή, 776 other;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                             Conservative 551;
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Pred. No. 6.3e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide D1876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 938 BP; 4 A; 144 C; 9 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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Example 6; Page 128; 159pp; English

RESULT 12

*М***ИМИМИМИМИМИМИМИМИ** 

a single surface

Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface

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                                                       Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses of a single surface
                                                                                                                                                                                                                                     Electron-transfer group; ETM; mismatch; genotyping;
gene expression; ss.
                                                                                                                                                                                                                                                               Oligonucleotide D1250:D1102
                                                                                                                                                                                                                                                                                               AAF58238;
                                                                                                                                          26~JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                    Synthet1c
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                                                                                                                                                                                                                                                                                                               AAF58238 standard;
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                                                                                                                                                                   26-JUL-2000; 2000WO-US20476
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                                                                                                                         (CLIN-) CLINICAL MICRO SENSORS
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)

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RESULT 14
AAF58238
ID AAF582
XX AAF582
XX AAF582
XX D1490
XX Elect
KW Elect
KW Elect
KW Gene
XX Synt)
XX O1-F
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                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression; ss
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17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide D1250:D1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1974 taagttaaatcaacatttttcagtaga
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   Sequence 244 BP; 19 A; 9 C;
                                                                                                                                                                                                                                                                                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLIN-) CLINICAL MICRO SENSORS
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                                                                                                                                                                                                                                                              Page 120;
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                                                                                                                                                                                                                                                           159pp; English.
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; Pred. No. 0.00036;
147; Mismatches 50;
12 G; 10 T; 194 other
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ARESULT ARAX331LT ARAX331L
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cc cell line into which an apoptosis resistance gene has been introduced.

CT he recombinant viruses generated are capable of expressing apoptosis-
cassociated genes. These can then be used in a variety of diseases for
cc which the induction of apoptosis by gene transfer, or where the
inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
care useful as vectors for gene therapy which can be applied to cancer
cc therapy for destroying cancer cells selectively, the treatment of
cc untoimmune diseases and graft rejection reaction, and apoptosis induction
ct therapy for inflammatory cells in inflammatory diseases. Prior arts have
cneountered the problem where if an ademovirus vector capable of
cexpressing an apoptosis-associated gene is introduced into animal cells,
ct the cells producing the virus will be destroyed because the period of
ct time required to induce cell death by apoptosis is shorter than that
crequired to replicate and produce the virus, resulting in failure to
obtain a recombinant virus having the integrated apoptosis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Base sequence of the plasmid pRx-ires-bsr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 38-41; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
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Best Local Similarity 46.0%; P
Matches 197; Conservative 0;
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RESULT 1 US-08-232-463-14/c US-08-232-463-14/c Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: RECOMBINANT FOWLPOX VIRUS PAPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: DORNER, F. APPLICANT: HOROLOGY & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria COUNTRY: USA APPLICATION NUMBER: US/07/935,313 FILING DATE: CLASSIFICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: D91114 300.6 FILING DATE: APPLICATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30,472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)63-4109 TELEPHONE: (703)63-410 TELECOMMUNICATION TON INFORMATION: STRANDEDNESS: single TOPOLOGY: 1.1. INFORMATION TONDOLOGY: 1.1. INFORMATION TON	ALIGNMENTS	c       28       41.4       1.7       6768       1       US-08-107-755A-1       Sequence         c       29       41.4       1.7       8457       1       US-08-544-332-1       Sequence         c       30       41.4       1.7       8457       2       US-08-998-416-385       Sequence         c       31       41.2       1.6       615       4       US-08-998-416-385       Sequence         c       32       41.2       1.6       615       4       US-08-998-416-385       Sequence         c       32       41.2       1.6       683       4       US-08-998-416-305       Sequence         c       34       40.8       1.6       658       4       US-08-998-416-305       Sequence         c       35       40.6       1.6       660       1       US-08-998-416-325       Sequence         c       36       40.4       1.6       660       1       US-08-998-416-325       Sequence         c       37       40.4       1.6       660       1       US-08-991-867B-32       Sequence         c       39       40.4       1.6       660       1       US-08-991-867B-32       Sequence

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Patent No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSON, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                               SOFTWARE: PatentIn Release #1.0, VGURENT APPLICATION DATA:
APPLICATION US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                            STREET: 620 Newport Center Drive CITY: Newport Beach
                                                                                                                                                                                                                           MEDIUM TYPE:
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5993827
                                                                                                                                                                                                                                                                                               California
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Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
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Wellems, Thomas E.
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Nowmort Center Drive 16th Floor
                                                                                                                                                                                                                       Floppy disk
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US-08-883-795A-36/c

Sequence 36, Application Patent No. 5985607 GENERAL INFORMATION:

US/08883795A

1674 15467

APPLICANT:

Delcuve, Gene Awang, Gregor

Genevieve

RESULT

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; MOLECULE TYPE: ; HYPOTHETICAL: NO ; ANTI-SENSE: NO US-08-487-826B-13
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                                                                                                               SEQUENCE CHARACTERISTICS:
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                   atattgcatgagagagatat 1694
                                                            atgcatgtcgttttcaaattcatatgatgaacgatccacgtaagtgctactactcctaca
                                                                                          aatagagttttcatgcaccag-tgttgatagtaacgtagtcgcggaatgtctaaaaacgat 1374
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                                            nucleic acid
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Pred. No. 0.003;
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ENERAL INFORMATION:

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US-08-487-826B-13; Sequence 13, Application US/08487826B; Patent No. 5993827
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; CLONE: Rh 32
US-08-883-795A-36
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                                                      RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 361-1398 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                        1055 tggtgaccacttaagtatttatatatcatgtatatatcttataggtatcatacaaaatgg 1114
                                                                                                                              1295 aaaaataatcgattaagagaaaata 1319
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                                                                                                                                                                                                                                                                                                                        1115 tcatgamacttttgcmatttcamtctmcttgttcattgtmgatgctmgcttttcmcatgt 1174
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REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   343 TATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAAATATTTAAT 284
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                            15361
                                                                                                                                                                                                                                                                                                                       15301 ATATATATATGTGTATGTATATGATTTTCTGTATATGTATTTGTGGGTTAAGGATATATA 15360
 15601
                                                                 15541
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19124 base pairs TYPE: nucleic acid
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 gaaacctccaaactatctaactaatacactcccatgtagaataaagaaaattatataaga 1923
                                                            tcgaccttcttatctttttcctctttattttatttttctcaggactttttttctacttaat 1863
                                                                                                                                                                                           Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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BINDING DOMAINS FROM PLASMODIUM VIVAX

AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS: 45
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 48.8; Di
Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 512;
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15660
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RESULT:
US-08-232-463-14

Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
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                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     STREET: 1000
CITY: Alexandria
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FTITING DATE: 26-AUG-1991
                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-0299
                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                    1800 Diagonal Road, Suite 500
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                                                                                                                                                                                                                                                                       Sequence 1, Application US/08446855A Patent No. 5849573
GENERAL INFORMATION:
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Best Local Similarity
Matches 22; Conserv
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INFORMATION FOR SEQ ID NO:
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                        APPLICANT: Stewart, Thomas S
APPLICANT: 'Flores, Maria V
APPLICANT: 'O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
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LENGTH: 7218 base pairs
                                                                                                                                                        NUMBER OF SEQUENCES:
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CLONE: pTZgpt-
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ZIP: 222
                                                                                                 CITY: Arlington STATE: Virginia
                   COMPUTER:
   OPERATING SYSTEM:
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                                                                                                                              STREET:
                                                                                                                                           ADDRESSEE:
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                                                                                            Virginia
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                                                                                 USA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/09150741
Patent No. 618396
GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                         2001 aacaaatattactgcaaaagtaggatcattatttttgtccaaa 2044
                                                                                                                                                                                                                                                                                                                                                                   1884 ctaatacactcccatgtagaataaagaaaattatatataagatattgttgatatttttgtaac 1943
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                                                                                                                                                                                                                                                                        Y Match 1.9%;
Local Similarity 44.5%;
hes 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 8920 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear.
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REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaagaagaaaagcgaaacccactaagccattacatgatatcgaccttcttatctttttc 1823
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                                                                                                                                                                                                    AAAAAGAAAAATGGGAAAAAATAATATAGATATATATAAATA 776
                                                                                                                                                                                                                                                                                                                                                TTTATTAATTTATTCATTTATTTATTTTTTTTTTAGTTATAAAATAGTAATTCTACTA
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GENERAL INFORMATION:

APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003

CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27

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                                US-09-007-005-17
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Sequence 17, Application US/09007005B Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1995-07-06 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8920
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1524 tttcatgtatttggcctatatataaacaaacatcgtaattatatacggatttttttcgga 1583
                                                                                                                                  2001 aacaaatattactgcaaaaagtaggatcattatttttgtccaaa 2044
                                                                                                                                                                                                                     1944 tagaaaatatatttg---ctctgtaatttttcgtaagttaaatcaacatttttcagtaga 2000
                                                                                                                                                                                                                                                                                     1884 ctaatacactcccatgtagaataaagaaaattatatataagatattgttgatatttttgtaac 1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1764 aaagaagaaaaagcgaaacccactaagccattacatgatatcgaccttcttatcttttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1704 aattttattttgaagaagaaataagagggaaggttacttgggtggatcgatgtgaaaaca 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1584 attitacgccatatctgtaagtatatataacatgcatgtcgttttcaaattcatatgatg 1643
                                                                                                                                                                                                                                                                                                                                                                              1824 ctctttattttttttctcaggacttttttctacttaatgaaacctccaaactatctaa 1883
                                                                                                        673 atgaacttgtatatgtaaatttataaatatttaaaacataaatataaatgtataaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 ttacttgaaatataaaacttattaatatatttccaattaatatgaatacaattattaata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.9%;
Local Similarity 44.5%;
mes 233; Conservative
                                                                                                                                                                                                                                                               tttattaatttattcatttatttatttttttttcttagtttataaaatagtaattctacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttttgatgtgtacacattaatatagttttacacttcttataataaaccatcctatatat 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atatatatatatatatatatatatatatatatatgtttgtgtgttcatttgtttataaaa
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Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                      552
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A
US-09-007-005-17
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                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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Best Local Similarity
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EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-244-796-17
                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 09/007,005 EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roberts, Richard W.
APPLICANT: LIU, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Szostak, Jack W.
                                                                                                                                                                                                                                                                                                                        ARLIER APPLICATION NUMBER: 60/064,491 ARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 289
TYPE: RNA
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                 TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILE REFERENCE: 00786/350007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                        OTHER INFORMATION: Translation template
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Translation template
                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 crurcrurgrcrgrcruaadaaaaaaaaaaaaaaaaaaaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 gtgggaaatctaaataagtgtagagaataataagtcctcaggtgggagattcaaagagag 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 ggttcgcatatacataaaccagtagacatatggataaafatgaacacacacaccaaaaaa 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 srnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnr 181
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10.8%; Pred. No. 0.1;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

03-JUN-1996

PCT/GB96/01332

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

02-JUN-1995

GB 9511196.9

REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:

TELEPHONE:

(703)

816-4100

REGISTRATION NUMBER:

32,955

620-29

Ms Mary J Wilson

SEQUENCE CHARAC

ERISTICS:

CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.25 (EPO)

APPLICATION NUMBER: FILING DATE: 01-DEC

UMBER: US/08/973,273 01-DEC-1997

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US-08-973-273-4/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 31;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08973273 Patent No. 6140085
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                      APPLICANT: Lister, Clare K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 gtgggaaatctaaataagtgtagagaataataagtcctcaggtgggagattcaaagagag 608
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                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      669 aattgaaacaagtaggattgaagaacaagaaacaaagaagcatgccc 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 srnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrcrargrcrurgrcrgrurarar 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 srnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnr 121
                                                                                                                                                 CITY: Arlington
                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virginia
                                                                                                                                                                    1: Nixon & Vanderhye P.C.
1100 No. 6140085th Glebe Road, 8th Floor
                                                                                                           United States of America
                                                                                                                                                                                                                                                                                              MacKnight, Richard
Bancroft, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                       Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9%;
                                                                                                                                                                                                                                                      Genetic Control of Flowering
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Pred. No. 0.1;
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DNA (genomic)

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US-08-998-416-535
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Best Local Similarity 52.0%;
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HYPOTHETICAL: NO
ANTI-SENSE: NO
TELEFAX: 919-54
NFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Brassica
                                                                                                                                                                                                                            SOFTWARE: PATENCE. CURRENT APPLICATION DATA: US/08/998,416
                                                                                                                                                                                APPLICATION NUMBER: UFILING DATE: 24-DEC-1CASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                  REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                         APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 GAATTTATATAAAAAAACGAATTTTATTTAATCAGTGAAAATTATATGTTATATTAAT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 gcatatatotaaatatgtocgaaactttcctacatactagaaaatatggagagttatgta 243
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                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3054 COLUMN PARK CITY: Research Triangle Park STATE: No. 6239264th Carolina
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                                  TELEPHONE:
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                          Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T: Wendland, Jurgen
T: Knechtle, Philipp
T: Rebischung, Corinne
INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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31-DEC-1996
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                                                                     PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46.8; DB Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                        SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072 tttatatatcatgtatatatcttataggtatcatacaaaatggtcatgaaacttttgcaa 1131
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ORIGINAL SOURCE:
                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1312 agaaaata 1319
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                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 TAATAGTCTACCCTTTAATTGGATATTACTACCTACTAAATATTTACCTAATAATATATT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 TAATATTAAGTGATATATATATTATATATATATATTTAATTTAATTTAATTTAACTTCATTGATATA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 TGATAATA 649
                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                               STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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nes 143; Conserv
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STRANDEDNESS: sing
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                                                        APPLICATION NUMBER: FILING DATE: 24-DE
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                 USA
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Knechtle, Philipp
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Steiner, Sabine
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                                                                                                               Release #1.0,
   CH 0016/97
                                                                            US/08/998,416
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                                                                                                                 Version
                                                                                                                 #1.30
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US-08-989-478-1/c
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Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08989478 Patent No. 5986082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                   COMPUTER READABLE FORM:
MEDLIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
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                                   CLASSIFICATION:
                                                        FILING DATE:
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                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                   27709
                                                                                                                                                                                                                              Research Triangle Park
No. 5986082th Carolina
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nilarity 48.5%;
Conservative
                                                                                                                                                                                                                  USA
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us 60/033,177
                                                                     US/08/989,478
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Pred. No. 0.62;
0; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF/5-30306/A/CGC1976
                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 782;
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US-08-989-478-1
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Best Local Similarity
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1474
                              1949
                                                            1534
                                                                                         1889
                                                                                                                                                                                               1769 agaaaaagcgaaacccactaagccattacatgatatcgaccttcttatctttttcctctt 1828
                                                                                                                    1594 AAGTTAAATTAGGATAAGATTTGTATGATTTTAAGTAAATTTACAATAACTCTCTATAAC 1535
                                                                                                                                            1654 ATAATAAGGTAAATAAATTATTGCTTTCCGCGTTTTTTACTTTTGTATTTCTTAAATGAT 1595
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                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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LOCATION: 3427..41
OTHER INFORMATION:
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AGTTTTCTTTAATTAATTTTTTAAAATGATATATATAAAATTTAATT
                         aatatatttgctctgtaatttttcgtaagttaaatcaacatttttcagt 1997
                                                                              acactcccatgtagaataaagaaaattatataagatattgttgatattttgtaactagaa 1948
                                                         TCAATAGCATCACATATTTAATTTAATTTACTAATTATCTTTTGAACAATTTTATGAAAT 1475
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4271..4474
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4586..4866
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                                                                                                                                                                                                                                                                                                                                  join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
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10-JAN-1997
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10-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Timothy
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10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBER: US 60/034,379
27-DEC-1996
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27-DEC-1996
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ID NO: 1
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Pred. No. 1
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                                                                                                                                                                                                                                          Mismatches 116;
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                                                                                                                                                                                                                                                                       DB 2;
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Application US/08996685

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COMPUTER READABLE FORM:
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                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
               TELEPHONE: (919) 541-8587
                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                                                              NAME: Meigs, J. Time
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                 CATION NUMBER:
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                                                                                                                                                                                                                                                                                    ATION NUMBER:
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DATE: 27-DEC-1996
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DATE: 27-DEC-1996
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ENTION: METHOD FOR PROTECTING PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruess, Wilhelm
Knauf-Beiter, Gertrude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ryals, John
Friedrich, Leslie
Uknes, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kessmann, Helmut
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                                                                                                                                                                                                           UMBER: US 60/035,022
10-JAN-1997
                                                                                                                                                                   10-JAN-1997
                                                                                                                                                                                                                                                                  JMBER: US 60/035,021
10-JAN-1997
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541-8689
                                                                          Timoth
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Best Local Similarity 49.3
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1654 ATAATAAGGTAAATAAATTATTGCTTTCCGCGTTTTTTACTTTTGTATTTCTTAAATGAT 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1769 agaaaaagcgaaacccactaagccattacatgatatcgaccttcttatctttttcctctt 1828
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                                                               CORRESPONDENCE ADDRESS
                                                                             UMBER OF SEQUENCES:
                                                                                                                               ITLE OF INVENTION:
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LOCATION: 4586..4866
OTHER INFORMATION: /
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LOCATION: 4271..4474
OTHER INFORMATION: /
                                                                                                 TLE OF INVENTION:
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CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME/KEY: exon
OCATION: 3427
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                               DDRESSEE: No. 6091004artis Corporation TREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                     aatatatttgctctgtaatttttcgtaagttaaatcaacatttttcagt 1997
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                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                            Application US/08880179
                                                                                                              INVENTION:
                                                                                                                                             Uknes, Scott
Jesse, Taco
Vos, Pieter
                                                                                                                                                                                                                          Delaney, Terry
Friedrich, Leslie
Weymann, Kristianna
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2787..3347
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                                                                                                              TRANSDUCTION CASCADE LEADING
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Pred. No. 1
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COMPUTER READABLE FORM:

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US-08-880-179-2
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Best Local Similarity 49.3
Matches 113; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                             1769 agaaaaagcgaaacccactaagccattacatgatatcgaccttcttatctttttcctctt 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                          1889 acactcccatgtagaataaagaaaattatataagatattgttgatattttgtaactagaa 1948
                                                                                                                                                     1594 AAGTTAAATTAGGATAAGATTTGTATGATTTTAAGTAAATTTACAATAACTCTCTATAAC 1535
                                                                                                                                                                                                                               1654 ATAATAAGGTAAATTAATTGCTTTCCGCGTTTTTTACTTTTGTATTTCTTAAATGAT 1595
                                  1949 aatatatttgctctgtaatttttcgtaagttaaatcaacatttttcagt 1997
                                                                          1534 TCAATAGCATCACATATTTAATTTTTACTAATTATCTTTTGAACAATTTTATGAAAT 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
1474 AGTTTTCTTTAATTAATTTTTTAAAATGATATATATAAAATTTAATT 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
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LOCATION: 2787..3347
OTHER INFORMATION: /
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LOCATION: 3427..4162
OTHER INFORMATION: //
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4271..4474
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TOPOLOGY: lin
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join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
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                                                                                                                                                                                                                                                                                                        Score 43.4; DB 3;
Pred. No. 1.1;
0; Mismatches 116;
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Search completed: November 22, 2001, 22:01:01 Job time: 29813 sec

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est2:*
em_estfun:*
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em\_estro1

em\_estro3

em\_estpl1

em\_estro4: em\_estro5: em\_estin4:

em\_estin5

em\_estin2:

em\_esthum27

em\_esthum15: em\_esthum16: em\_esthum17: em\_esthum18: em\_esthum19: em\_esthum20:

em\_estom1
em\_estom2
em\_estov1
em\_estov2
em\_estov2

em\_estro12:
em\_estro13:
em\_estro14:

em\_estro9

em\_estro8:

em\_estro18

em\_estro15

gb\_est41:\*
gb\_est42:\*
gb\_est43:\*
gb\_est44:\*

gb\_est48:\*
gb\_est49:\*
gb\_est50:\*

gb\_est53:

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em_gss_rod6:*
em_gss_rod7:*
em_gss_rod8:*
gb_gss35:*
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gb\_est69: \*
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gb\_est72: \*
gb\_est73: \*
gb\_est74: \*
gb\_est91: \*
gb\_est94: \*
gb\_est97: \*
gb\_est98: \*

gb\_est106 gb\_est67:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb\_est107:\*
gb\_est108:\*
gb\_est109:\*

em\_estro22:\*
em\_estro23:\*
em\_htc:\*

em\_esthum33:\*
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em\_estpl11:\*

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em\_esthum30:\*
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CNSO039G 1101 bp DNA GSS 03-JUN-1999  Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK08K10 of RFCI-98 lbbrary from Drosophila melanogaster (fruit fly), genomic survey sequence.  NALO63921 alignitude and sequence.  NALO63921 alignitude and sequence.  SSS.  Fruit fly.  Fruit fly.  Fruit fly.  Brosophila melanogaster  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa; Arthropoda; Diptera; Brachycera; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  E 1 (bases 1 to 1101)  S Genoscope.  Dlirect Submission	.7 1443 167 BE421656 BE4216	2.7 1101 219 CNS0182P AL108811 2.7 873 220 CNS024M5 BG520365 2.7 915 154 BG520365 BG520365 2.7 1101 219 CNS0145U AL103740 2.7 1101 219 CNS0145U AL201604 2.7 1101 219 CNS00LJT AL068307 2.7 1101 219 CNS0105X AL068307 2.7 1101 219 CNS0105X AL068307 2.7 1101 219 CNS0105X AL068307 2.7 1068 219 CNS016TV AL068307	2.7 959 219 CNS00655 2.7 1029 220 CNS0120M 2.7 1096 256 B09949 2.7 1096 256 B09949 2.7 1001 219 CNS01400 2.7 987 219 CNS014PQ 2.7 1001 219 CNS014PQ 2.7 1010 219 CNS002PG 2.7 987 219 CNS00418 2.7 1010 219 CNS00418 2.7 1101 219 CNS017V2 2.7 AL108336	2.9 928 219 CNSOODKY 2.9 928 219 CNSOODKY 2.9 100 219 CNSOOPH 2.9 1101 219 CNSOO21J 2.8 1101 219 CNSOO1FB 2.8 1101 219 CNSOO1FB 2.8 997 219 CNSOO1FB 2.8 1101 219 CNSOO26Z 2.8 1101 219 CNSOO26Z 2.8 1101 219 CNSOO26Z 2.8 1101 219 CNSOO0X 2.8 1101 219 CNSOOX 2.8 1101 219 CNSOO0X 2.8 1101 219 CNSOOX 2.8 1101	.5 1101 219 .4 1101 219 .3 1101 219 .3 1101 219 .1 1001 219 .1 1001 219 .1 1001 219 .1 1101 219 .1 1101 219 .1 1101 219 .1 1101 219 .1 1002 220 .1 1101 219 .1 1043 219 .0 1101 219	SUMMARIES Query Match Length DB ID D
Db 736 GRKWRRTWKR  Qy 1812 cttatctttt  ::::   Db 676 DRTDAWWADA   Oy 1872 caaactatct   Oy 1872 caaactatct   Oy 1873 atattttgta   Oy 1932 atattttgta   Oy 1932 atattttgta   Ob 556 WAARAAWWAW	2 attcatatgatgaacgatccacgtaagtgctactactcctacaatattgcatgagagaga	Oy 1512 acacttggttggtttcatgtatttggcctatatataaacaaac	Qy 1392 gattggttagaattggtattagtaggacattctaactttttgttagtctgttgatttag 1451 ::::::::::::::::::::::::::::::::::	### According to Septime Herein Sept	melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library of filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.	JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                               EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/clone_lib="RPCI-98"
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                                               /organism="Drosophila melanogaster"
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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3.3%; Score 81.8; DB 219;
Local Similarity 19.1%; Pred. No. 1.2e-05;
hes 125; Conservative 291; Mismatches 215;
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                                                                                                                     taaatcaacatttttcagtagaaacaaatattactgcaaaaagtaggatcattatttttg 2038
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ALO69706
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/db_xref="taxon:7227"
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Matches Query Match Best Local :

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Conservative

101;

Mismatches

454;

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Gaps

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Similarity

33.18;

Score 77.6; Pred. No. 7.

DB 219; 7.6e-05;

Length 974;

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pand bot the ST libraries. A more detailed description of the library
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                                                                  /organism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
/clone_lib-"ReCI-98"
/clone-"BACR37D06"
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Drosophila melanogaster genome survey sequence T7 end of E
BACR13009 of RPCI-98 library from Drosophila melanogaster
 Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                        Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                                                                       Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom.
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleosta
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 1092)
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Human gene number estimate provided by genome wide analysis using Tetracoon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="222L11"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BACN37F08 of DrosBAC library from Drosophila me
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (Dases 1 to 1101)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis.
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Similarity 38.6%;
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/clone_lib="G"
/note="Genoscope sequence ID :
/note="Genoscope sequence ID :
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/db_xref="taxon:99883"
/clone="222L11"
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Pred. No. 0.00019;
8; Mismatches 221;
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113 others
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RESULT 12
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Best Local Similarity 37.3
Matches 203; Conservative
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                                                                                                                                                                                       TTTTTTTTTTTTTTTTTTTTWTWTWTATWTWATATATWTARRGGRAADDAAAAAAAA
                                                                                                             Drosophila melanogaster genome survey sequence T7 end of BAC BACN11G11 of DrosBAC library from Drosophila melanogaster (frufly), genomic survey sequence.

ALL03735. 1 GI:5615346
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope
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/plasmid-"pBeloBAC11"
/db_xref-"taxon:7227"
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/note="end : T7"
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pBeloBAC11
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/clone="BACN15M24"
/note="end : T7"
a 87 c 79 g
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/plasmid="pBeloBAC11"
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                                                                                                                                                                                                               Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069706
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila. melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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/clone="BACR29B23"
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## SUMMARIES

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                       Submitted (03-MAR-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.blochem.mpg.de mayer@mips.blochem.mpg.de Project Coordinator: Mike Beven, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can by viewed at: http://websyr.mips.blochem.mpg.de/proj/thail/.
                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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                                                                                                    EU Arabidopsis sequencing, project.
Direct Submission
                                                                                                                                        Bevan, M., Koetter, P., Hempel, S., Entian, K.-D., Mewes, H.W., Mayer, K.F.X. and Schueller, C.
                                                                                                                                                                                          Arabidopsis thaliana
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|15334. 15577,1591. 15798,15956. .16078)
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DEFINITION
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ATCHRIV87 196339 bp I Arabidopsis thaliana DNA AL161591 AL161591.2 GI:7270703 DNA chromosome 4, PLN contig fragment No. 16-MAR-2000 |ment No. 87

REFERENCE AUTHORS Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 42610 to 143618; 123423 to 196339)
Rose,M., Hempel,S., Entian,K.-D., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
Unpublished

JOURNAL REFERENCE AUTHORS TITLE 2 (bases 1 to 196339)
EU Arabidopsis sequencing, project.
Direct Submission

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Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

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Location/Qualifiers
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contains EST gb:AW033651.1, W43270, AA728669, T42795, Z37671, AI100742, AA395771, AA657303, T41871, T45633
                                                                  Nnote="strong similarity to cold acclimation protein MCOR413, Triticum asstivum, PATCHX:G1657855 Contains Prokaryotic membrane lipoprotein lipid attachment site AA147-157
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/gene="AT4g37220"
Join(8876. .9051,9141. .9248,9330. .9400,9486. .9739)
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/variety="Columbia"
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/chromosome="4"
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                                                                                                                                                           'gene="AT4g37220"
                                                                                                                                                                                                                                                                                                                                     'gene="AT4g37210"
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gene-"AT4g37210"
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gene-"AT4g37210"
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                         AA650647, AI996990.1, T42949, AA040998,
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/translation="MEFANPYKVGYVLLKYPMCFICNSDDMDFDDAVAAISADEELQL
GQIYFALFLCWLRQFLKAEEMAALAVKASSALMRGGGGCRRKCVEFIVSDKLRWRVG
SGDDTVGSGSGRKVRNGDGGGSVSSSRRRKCYAAELSTIDE"
21559. .23955
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/gene="AT4g37230"
10194. .10398
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                                                                               /product="putative protein"
/protein_id="CAB80390.1"
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1188-51200, 5' part of gene couldn't be reconstructed,
osssible pseudogene, no ATG
strong similarity to photosystem II oxygen-evolving
complex protein 1, spinach, PIR2:A23626
contains EST gb: 234685"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oin(10194. .10398,11131. .11357)
gene="AT4g37230"
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gene="AT4g37220"
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                                                                                                                                                                           note="contains
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gene="AT4g37230"
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protein_id="CAB80389.1"
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Jene="AT4g37220"
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Jene="AT4g37220"
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34372. .35334
/gene="AT4g37260"
34372. .35334
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NLTVVSLENNYFSGEIPGGWRVVEFFLDLSSNIGHNSFFFFGSUNGSLQVLNYSFNQISG
EIPPEIGVNFFRNYTVDLSFNNLTGEPIPDSAVFLNQESNFFFGRNPGLLGFFRNPCTL
PSSPSIVSEADVPTSTPAIAAIPNTIGSNPVTDDNSQOTDPNFTGLRFGVIIGIVVG
DIAGIGILAVIFLYIYRCKKKIVDNNNNDKQRTENDTITLSTFSSSSSSPEESRRFR
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/gene="AT4g37250"
/note="similarity to protein kinase TMK1, receptor type
precursor - Arabidopsis thaliana, PIR1:JQ1674
contains EST gb:H76836"
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/number=1
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyeera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 4601)
Lewis, D.L., Farquhar, A.L. and Kaguni, L.S.
Sequence, Organization and Evolution of the A+T Region of
Drosophila melanogaster Mitochondrial DNA
Mol. Biol. Evol. 11, 523-538 (1994)
Kaguni, L.S.
Direct Submission
Submitted (28-JUN-1994) Laurie S. Kaguni
Biochemistry, Michigan State University,
48824-1318, USA
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Drosophila melanogaster
U11584
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Dorner, F., Scheifilnger, F. and Falkner, F.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                    fruit fly.
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                                                                                                                                                                                                                               aggtatcatacaaaatggtcatgaaacttttgcaatttcaatcttacttgttcattgtaga 1156
           ctcttacactaatttcttaaaaataatcgattaagagaaaatagagttttcatgcaccag
                                                                                                             tttgttggtcaacgtttaatttcttgattattgatgtcaaaaattcagagcgttcagaa 1276
                                                                                                                                                                                     tgctagcttttcacatgttttgaaaattagtctggatctgaaattctttaattagcattg 1216
                                                                                                                                                                                                                  TTTTATTATATAAATATTTTTTATAAAAATAATACATTTAAGAAATTTTTAAAAAAATTTA
                                                                                                                                                                                                                                                                  tgttgatagtaacgtagtcgcggaatgtctaaaacgattatgagtttggtgttttgattg 1396
                                                              ATTAAATTAATAAATAAATATGAGAATATAAATTTTATAAATTATATCTACATTTT
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/organelle="mitochondrion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3577. .4040
/note="repeat II-B2"
/rpt_type=tandem
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2649. בזוור
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2512. .2648
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rpt_type=tandem
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                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"repeat II-C"
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Pred. No. 0.00081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1749 atcgatgtgaaaacaaaagaagaaaaagcgaaacccactaagccattacatgatatcgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2658 TTTTTATAAAAATAATACATTTAAAAATTTTTAAAAAATTTATATATAATTTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTATTATAAAAATTTTTTTTTTTTAAAAAAACATGATTTTATTATATAAAAATA
                                                                                                                                                                                                                                                                                               cttcttatctttcctctttatttttctcaggacttttttctcacttaatgaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtaaa--gagtotttttattttacaccagttgagacttgggatcgatagtacttgaaaca 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctccaaactatctaactaatacactcccatgtagaataaagaaaattatata-agatatt 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tttttcggaattttacgccatatctgtaagt----atatataacatgcatgtcgtttt 1628
                                                                                                                           AAATAATTTTATTAAAATAA
                                                                                                                                               ataaaaactcacaaatccaccaa
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                      U37541.1
fruit fly
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                                              DNA circular INV complete mitochondrial
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2047 2239 1987 2299

1940

2224

1999

2164 2119 2104

2059

2359

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2479

1808

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C-"cytochrome c oxidase subunit I"
1.1d="AAC47812.2"
1.1d="AAC4781
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L="AAC47811.1"
L="14":1AAC47811.1"
L="16530"
L: 1916530"

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.1472.1474...3009)
hanism underlying reading frame shift after
n uncertain"
rt=1
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d="AAC47814.1"
GI:1166533"
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tRNA-Ile"
(97. .165)
tRNA-Gln"
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LLHGQLIEMIWTILPAIILLFIALPSLRLLYLLDEINEPSVTLKSIGH
FNNIEFDSYMIFTNELMTDGFRLLDVDNRVVLPMNSQIRILVTAADVI
KVDGTPGRLNQTNFFINRPGLFYGQCSEICGANHSFMPIVIESVPVNY
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1-"AAC47813.1"
31:1166532"
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(1322. .13
n-"MPQMAPISWLLLFIIFSITFILFCSINYYSYMPNSPKSNELKNI
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Query Match
Best Local S
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      17874
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  ATTAAATTAATAATAAATAATATGAGAATATAAATTTTTATAAATTATATCTACATTTT
                                                                                                                                                                                                                                                                                                                                                              totatgttactatgtaaatggtgaccacttaagtatttatatatcatgtatatatcttat 1096
                                      ctcttacactaatttcttaaaaataatcgattaagagaaaatagagttttcatgcaccag 1336
                                                                                                                                                                 TTTTATTATAAAATATTTTTTATAAAAATAATACATTTAAGAAATTTTTAAAAAAATTTA 1799:
                                                                               ttttgttggtcaacgtttaatttcttgattattgatgtcaaaaattcagagcgttcagaa 1276
                                                                                                                                                                                                     tyctagetttteacatgttttgaaaattagtetggatetgaaattetttaattageattg 1216
                                                                                                                                                                                                                                                                                                                                566;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6401. .8124)
/note="TAA stop codon is completed by the addition of residue to the mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MFSIIFIALLILLITTIVMFLASILSKKALIDREKSSPFECGFD
PKSSSRLPFSLRFFLITIIFLIFDVEIALILPMIIIMKYSNIMIWTITSIIFILILLI
GLYHEWNQGMLNWSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"tRNA-Gly"
5608. .5961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MSTHSNHDFHLYDYSPWPLTGAIGAMTTVSGMVKWFHQYDISLF
VLGNIITILTVYQWWRDVSREGTYQGLHTYAVTIGLRWGMILFILSEVLFFVSFFWAF
FHSSLSPAIELGASWPPMGIISFNPFQIPLLNTAILLASGVTVTWAHHSLMENNHSQT
TQGLFFTVLLGIYFTILQAYEYIEAPFTIADSIYGSTFFMATGFHGIHVLIGTTFLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mmtnlfsvfdplaifnfslnwlstflgllmipsiywlmpsryni
mwnsilltlhkefktllgpsghngstfifislfslilfnnfmglfpyiftstshltlt
LSLALPLWLCfmlygwinhtqhmfahlvpqgtfailmffmvciftisniirpgtlavr
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/protein_id="AAC47817.1"
/db_xref="GI:1166536"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="cytochrome c oxidase
/protein_id="AAC47816.1"
/db_xref="GI:1166535"
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/protein_id="AAC47815.1"
/db_xref="GI:1166534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="tRNA-Phe"
complement/f/^
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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₹ <b>♣</b>	FEATURES source		COMMENT	TITLE JOURNAL			TITLE JOURNAL REFERENCE AUTHORS		REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Homo sapiens" /db_xref="taxon:9606" /clone="RP11-72A1"	Location/qualifiers 1176174	hitehead de: WIBR http://N sequence - Project oject nar one name	On Dec 24, 2000 this sequence version replaced gi:11597092.  All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  Direct Submission Submitted (27-DEC-2000) Whitehead Institute/MIT Center for Genome Passarch (27-DEC-2000) Whitehead Institute/MIT Center for Genome	McPheeters, R., Meldrim, J.; Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Ngyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Rise, C., Rogov, P., Roman, J., Rosetti, M., Ribeack, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuer, S., Schauer, S., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stolanovic, N., Stolanovic, N., Stolanovic, N., Sougnez, C., Spencer, B., Stange-Thomann, N., Stolanovic, N	Barna, N. Bastien, V. Boguslavkly, L., Boukhgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., Larcoque, K., Lamazares, R., Landers, T., Lechoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marchis, N., Marthews, C., McCarthy, M. McCaran, D., Macdonald, P., Marchis, M., Marthews, C., McCarthy, M. McCaran, D., Macdonald, P., Macdonis, N., Matthews, C., McCarthy, M. McCaran, D., McCaran, V.	Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M. Direct Submission Submitted (05-MAY-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 176174) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,	Baldwin,J., Barna,N., Beckerly,R., Benn,J., E Cerny,J., Colangelo,M., Collins,S., Collymor DeArellano,K., Depayre,E., Devon,K., Dewar,K., Doyle,M., Ferreira,P., FitzHugh,W., Forrest Gages,D., Galagan,J., Gardyna,S., Gilbert,D., Heaford,A., Horton,L., Howland,J.C., Jones,C., Lehoczky,J., Lieu,C., Locke,K., Macdonald,F., McEwan,P., McGurk,A., McKernan,K., McLaughil, Molla,M., Morris,W., Morrow,J., Mychaleckyj Niloff,M., O'Connor,T., O'Donnell,P., Pavlin, Pollara,V., Riley,R., Roberts,D., Roy,A., Menn,N., Stojanovic,N., Stone,C., Subramanian Torruella-Miller,I., Vassiliev,H., Vo,A., W		Ordata; Craniata; Vertebrata; E

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complement(4034. 9553)
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complement(29996..30092)
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30093..30154
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complement(20126. .23)
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                         gagagagatatgtattataaattttatttgaagaagaaataagagggaaggttacttg
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                                                                                                                                                                                                                                                                                         TAAATATATCAATATAATAGATACATTATATAT---AATAAATATATCAATATATAAT
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gaaacctccaaactatctaactactacactcccatgtagaataaagaaaattatataaga 1923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented from the T7 to the SP6 end.
                                                                                                                                                                                                                      - Web : www.genoscope.cns.fr)
On Nov 20, 2000 this sequence version replaced gi:10944764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS05TCG 165097 bp DNA HT0
Homo sapiens chromosome 14 clone R-204N11,
                                                                                                                                             Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                            Center: Genoscope / Centre National de
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                            IMPORTANT: This sequence is unfinished and does not necessarly
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191 91006 EVRY cedex - FRANCE (E-mail :
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gtaaagagtcttttattttacaccagttgagacttgggatcgatagtacttgaaacact 1516
                                      gttagaattggtattagtaggacattctaacttttttgttagtctgttgatttaggatgc 1456
                                                                                                                   ATTTTTTATAAATATA-
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                                                                                                                                                                                                                                                             ATATTTTATAAAATATATTTTATGTATATATTTTATAAAATATATATTTTATGTATAT 77234
                                                                                                                                                                                                                                                                                  ttttgttggtcaacgtttaatttcttgattattgatgtcaaaaattcagagcgttcagaa 1276
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                                                                                                                                                                                                                                                                                                                                                                      tgctagcttttcacatgttttgaaaattagtctggatctgaaattctttaattagcattg 1216
                                                                                                                                                                                                                                                                                                                                                                                                             Percentage of bases with a quality value >= * NOTE: This is a 'working draft' sequence * This sequence will be replaced * by the finished sequence as soon as it is * the accession number will be preserved.
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/db_xref="taxon:9606"
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Pred. No. 0.0025;
0; Mismatches 652;
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On Mar 22, 2001 this sequence version replaced g1:12963041.
                                                       2 (bases 1 to 183250)
Waterston, R.H.
Direct Submission
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          1 (bases 1 to 183250)
Waterston, R.H.
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                             AC012492
                                                                                               Unpublished
                                                                                                                                                                                                                       AC012492.8 GI:13431121
                                                                                                                                                                                                                                         HTG omo sapiens chromosome UNK clone RP11-224B10, IEQUENCE, 2 unordered pieces.
                                                                                                            sequence of Homo sapiens
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 g1:12963041
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Summary Statistics
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Insert size: 183150; sum-of-contigs
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Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
2 (bases 1 to 879)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Di Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
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O'Connor, T., O'Donnell, P., O'Nell, D., Ollver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovič, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Submitted (27-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 24, 2000 this sequence version replaced gi:11597092. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Smit, A.F.A. & Green, P. (1996-1997) Smit, A.F.A. et Green, P. (1996-1997) Smit, A.F.A. & Green, P. (1996-1997) Smi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum Homo sapiens, clone RP11-72A1
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Contact: sequence_submissions@genome.wi.mit.edu
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Center project name: L642
Center clone name: 72_A_1
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Canavalia.
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                                                                                                                                                                                       Submitted (10-NOV-1999) Biology, Seoul National University, 56-1, Sinrim-Dong, Kwanak-Gu, Seoul 151-742, Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       YOO, S.K., Lee, Y. and Kwon, Y.M. Properties of ornithine carbamoylases lineata leaves and their cDNA cloning
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latsaapqkygoknflhldedkdtilkmldbaleyksllksgortrrpfegktwsmi
ftkpsmrtryfettgghaiylgdddlomkkeetgretgryndiimarvy
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2 (bases 1 to 192929)
4 Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
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Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J.,

Kurdi,O.B., Conway,A.B. and Davis,R.W.

Plasmodium falciparum 3D7 chromosome 12
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Eukaryota; Alveolata; Apicomplexa;
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                                                                                                                                                                                                                                                                                                                                                                                                                             by the finished sequence as soon as it is available the accession number will be preserved.

1 192929: contig of 192929 bp in length.
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                                                                                                                                                                                                                                                                                                                                             /organism="Plasmodium
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RESULT 1
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misc_feature
                                                                       misc_feature
                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 185400; sum-of-contigs
Insert size: 175198; 7.5% error; agarose-fp
Quality coverage: 11.67x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reconsensus quality: 184826 bases at least Q40 Consensus quality: 185039 bases at least Q30 consensus quality: 185156 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 1008 of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Mar 20, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome 10 clone PROGRESS ***, 5 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: humguery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: bA462F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coverage: 12.35x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                   1 27247: contig of 27247 bp in length
27248 27347: gap of 100 bp
27348 29385: contig of 2038 bp in length
29386 29485: gap of 100 bp
29486 122834: contig of 93349 bp in length
122835 122934: gap of 100 bp
122835 160240: contig of 37306 bp in length
160341 185800: contig of 25460 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rect Submission
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                  /note="assembly_fragment:00683
fragment_chain:1"
                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
ob_xref="taxon:9606"
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actaagccattacatgatatcgaccttcttatctttttcctctttattttatttttctca 1844
                                                  taagagggaaggttacttgggtggatcgatgtgaaaacaaaagaagaaaaagcgaaaccc 1784
                                                                                tataacatgcatgtcgttttcaaattcatatgatgaacgatccacgtaagtgctactact 1668
                                                                                                                                                                                                                camacatcgtaattatatacggatttttttcggaattttacgccatatctgta-agtata 1608
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fragment_chain:1"
122935_ .160240
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| 43562 c 40961 g
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clone_end:T7
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Best Local :
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2057 tatagggitgtagtaaaaacaaaacacattcitgattigccccaaaaaataaagagagag 2116
                                                                                                                                            1939 gtaactagaaaatatatttgctctgtaatttttcgtaagttaaatcaacatttttcagta 1998
                                                  630 AATTAAAATAACATCATCAACATCTTTAATCATCTACATCCAACCTGATAATATGA
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Local Similarity 47.2%;
                                                                                 gaaacaaatat--tactgcaaaaagtaggatcattatttttgtccaaaatctcagttagc
                                                                                                                   taatttttcgtaagttaaatcaacatttttcagtagaaacaaatatt 2010
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S96842
S96842.1 GI:248952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein binding and DNase-I-hypersensitive sites in the cis-acting regulatory region of the spore-coat SP96 gene of Dictyostelium Mech. Dev. 36 (3), 105-115 (1992) 92239372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum prespore cells Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 96842] from the original journal article. This sequence comes from Fig. 2.
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Tasaka,M., Hasegawa,M., Nakata,M., Orii,H., Ozaki,T. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Sp96"
/gene="spore-coat protein; Initiation codon starts at
/note="spore-coat protein; Initiation codon starts at
nucleotide 182"
nucleotide 182"
153 c 228 g 992 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Dictyostellum discoideum"
/db_xref="taxon:44689"
2247. .2305
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155 AATTGTTTTAAAAGAAAAGATAAA
                                                                                                                                     274 AATGTATCAACATCATCAAC-TACAACAACCACCACCACCACCACAACAACAACAACAAC
                                                                                                                                                                                                                                                                                 570 TGGAAAGATCTAGAAAGCATCGTGCACTTTCAATTACACCACATAAACAAAAACAGTATA 511
                  ttcttattcattaaaaaaaaaaaa 2500
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                                                                    AACATCAACAACATAATCATGAATCAAATGAAAGAAGTAATCAACTATTAGAATCATT 156
                                                                                                  aatatacacaacaagtattaaatcttagatattgtgggtctccctttcttctattcatt 2476
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132
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Search completed: November 22, 2001, 22:16:10 Job time: 31672 sec

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REFERENCE
AUTHORS
TITLE
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AUTHORS
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                                                                                                       Submitted (03-MAR-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
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Arabidopsis
project).
AL035605
AL035605.1
                                            Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                     2 (bases 1 to 91740)
EU Arabidopsis sequencing, project.
Direct Submission
                                                                                                                                                                                                                                                                                                                   Bevan,M., Koetter,P., Her
Mewes,H.W., Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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AL355100 Homo sapi
AC083827 Homo sapi
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                                                                         number-
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join(5135. .5350,5437.
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Contains Peroxidases
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LFTDRRSKPTVDLMANNGQLFNQAFINSMIKLGRYGVKTGSNGNIRRDCGAFN"
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navokkvqqtettipatiriyehdcevngcdasvmiastnnnkaekdheenisilagdg
edtvikakealdavencrnkyscadiitmatrdvvnilaggeqydveigridgisstaa
Syggklphptddvnkltsleakngisindmialsgahfilgeahctkvenriytenktt
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'variety="Columbia"
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5893. .60
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/note="similarity to predicted protein, Arabidopsis
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complement(9998. .10536)
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methylotrophus, PIR2:S74213
contains EST gb:T46402, AA404801, T22522"
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/gene="F19F18.30"
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/AGLMSFISSYPEL"MSCLAFQSLLFEA.GGTVPMPVGA/MGMLWTWRNWHYCQAAVETVL
RGGTLRFISDLLESPSLMISCDESSEIWHQDYSRNQTHACRTSTSRST;EMKDSLVNR
KRLKSDSDLDLQVNHGLTLTAPAVPVPFLPPSSFCKVVKGDRPGSPSEESVTTSCWEN
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C 62180	CACATGATGCTGATGCAATATACACAAACAAAGTATTAAATCTTAGATATTGTGGGTCTCC	62121	В
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T 61880	AAAAATAAAGAGAGAGAAGAATATTGTTCAAAAAGTGGTCTCTTCTCTCTC	61821	ģ
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r 61580	ATATCGACCTTCTTATCTTTTCCTCTTTATTTTTTTCTCAGGACTTTTTTCTACTT	61521	ф
ר 1860	atatégacottottatottrttcototttattttatttttctcaggactttttttctactt	1801	Qy
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE RESULT ATCHRIV87

JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS ATCHRIV87 196339 b Arabidopsis thalian AL161591 AL161591.2 GI:7270 Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Trache
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 42610 to 143618; 123423 to 196339)
Rose,M., Hempel,S., Entian,K.-D., Mewes,H.W.,
Mayer,K.F.X.
Unpublished 2 (bases 1 to 196339) EU Arabidopsis sequencing, project. Direct Submission Submitted (10-MAR-2000) MIPS, at the thale cress. đđ DNA chromosome 4, Embryophyta; Trachedons; core eudicots; Tracheophyta; Spermatophyta; dicots; Rosidae; eurosids II; contig Σ. 16-MAR-2000 fragment No. 87 Lemcke, K.

Max-Planck-Institut